



## SEQUENCE LISTING

<110> KAO CORPORATION  
Okuda, Mitsuyoshi  
Izawa, Yoshifumi  
Kobayashi, Tohru  
Koyama, Shingo  
Sato, Tsuyoshi

<120> ALKALINE PROTEASE

<130> 251701-US0

<140> 10/820,712

<141> 2004-04-09

<150> 2003-106708

<151> 2003-04-10

<160> 23

<170> PatentIn version 3.2

<210> 1

<211> 434

<212> PRT

<213> Bacillus sp. KSM-KP43

<400> 1

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser  
1 5 10 15

Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly  
20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly  
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp  
50 55 60

Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly  
65 70 75 80

Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser  
85 90 95

Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln  
100 105 110

Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn  
115 120 125

Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn  
130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala  
145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala  
165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe  
180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg  
195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly  
210 215 220

Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe  
225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met  
245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe  
260 265 270

Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala  
275 280 285

Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn  
290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr  
305 310 315 320

Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser  
325 330 335

Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser  
340 345 350

Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu  
355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp  
 370 375 380

Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu  
 385 390 395 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val  
 405 410 415

Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile  
 420 425 430

Val Asn

<210> 2  
 <211> 1923  
 <212> DNA  
 <213> Bacillus sp. KSM-KP43

<220>  
 <221> CDS  
 <222> (1)..(1920)

<220>  
 <221> sig\_peptide  
 <222> (1)..(618)

<220>  
 <221> mat\_peptide  
 <222> (619)..()

<400> 2	
atg aga aag aag aaa aag gtg ttt tta tct gtt tta tca gct gca	45
Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala	
-205 -200 -195	
gcg att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt	90
Ala Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly	
-190 -185 -180	
gca agg aat ttt gat ctg gat ttc aaa gga att cag aca aca act	135
Ala Arg Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr	
-175 -170 -165	
gat gct aaa ggt ttc tcc aag cag ggg cag act ggt gct gct gct	180
Asp Ala Lys Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala	
-160 -155 -150	
ttt ctg gtg gaa tct gaa aat gtg aaa ctc cca aaa ggt ttg cag	225
Phe Leu Val Glu Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln	
-145 -140 -135	
aag aag ctt gaa aca gtc ccg gca aat aat aaa ctc cat att atc	270
Lys Lys Leu Glu Thr Val Pro Ala Asn Asn Lys Leu His Ile Ile	

-130	-125	-120	
caa ttc aat gga cca att tta gaa gaa aca aaa cag cag ctg gaa			315
Gln Phe Asn Gly Pro Ile Leu Glu Glu Thr Lys Gln Gln Leu Glu			
-115	-110	-105	
aaa aca ggg gca aag att ctc gac tac ata cct gat tat gct tac att			363
Lys Thr Gly Ala Lys Ile Leu Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile			
-100	-95	-90	
gtc gag tat gag ggc gat gtt aag tca gca aca agc acc att gag cac			411
Val Glu Tyr Glu Gly Asp Val Lys Ser Ala Thr Ser Thr Ile Glu His			
-85	-80	-75	-70
gtg gaa tcc gtg gag cct tat ttg ccg ata tac aga ata gat ccc cag			459
Val Glu Ser Val Glu Pro Tyr Leu Pro Ile Tyr Arg Ile Asp Pro Gln			
-65	-60	-55	
ctt ttc aca aaa ggg gca tca gag ctt gta aaa gca gtg gcg ctt gat			507
Leu Phe Thr Lys Gly Ala Ser Glu Leu Val Lys Ala Val Ala Leu Asp			
-50	-45	-40	
aca aag cag aaa aat aaa gag gtg caa tta aga ggc atc gaa caa atc			555
Thr Lys Gln Lys Asn Lys Glu Val Gln Leu Arg Gly Ile Glu Gln Ile			
-35	-30	-25	
gca caa ttc gca ata agc aat gat gtg cta tat att acg gca aag cct			603
Ala Gln Phe Ala Ile Ser Asn Asp Val Leu Tyr Ile Thr Ala Lys Pro			
-20	-15	-10	
gag tat aag gtg atg aat gat gtt gcg cgt gga att gtc aaa gcg gat			651
Glu Tyr Lys Val Met Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp			
-5	-1 1	5	10
gtg gct cag agc agc tac ggg ttg tat gga caa gga cag atc gta gcg			699
Val Ala Gln Ser Ser Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala			
15	20	25	
gtt gcc gat aca ggg ctt gat aca ggt cgc aat gac agt tcg atg cat			747
Val Ala Asp Thr Gly Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His			
30	35	40	
gaa gcc ttc cgc ggg aaa att act gca tta tat gca ttg gga cgg acg			795
Glu Ala Phe Arg Gly Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr			
45	50	55	
aat aat gcc aat gat acg aat ggt cat ggt acg cat gtg gct ggc tcc			843
Asn Asn Ala Asn Asp Thr Asn Gly His Gly Thr His Val Ala Gly Ser			
60	65	70	75
gta tta gga aac ggc tcc act aat aaa gga atg gcg cct cag gcg aat			891
Val Leu Gly Asn Gly Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn			
80	85	90	
cta gtc ttc caa tct atc atg gat agc ggt ggg gga ctt gga gga cta			939
Leu Val Phe Gln Ser Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu			
95	100	105	
cct tcg aat ctg caa acc tta ttc agc caa gca tac agt gct ggt gcc			987
Pro Ser Asn Leu Gln Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala			
110	115	120	

aga att cat aca aac tcc tgg gga gca gca gtg aat ggg gct tac aca Arg Ile His Thr Asn Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr 125 130 135	1035
aca gat tcc aga aat gtg gat gac tat gtg cgc aaa aat gat atg acg Thr Asp Ser Arg Asn Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr 140 145 150 155	1083
atc ctt ttc gct gcc ggg aat gaa gga ccg aac ggc gga acc atc agt Ile Leu Phe Ala Ala Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser 160 165 170	1131
gca cca ggc aca gct aaa aat gca ata aca gtc gga gct acg gaa aac Ala Pro Gly Thr Ala Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn 175 180 185	1179
ctc cgc cca agc ttt ggg tct tat gcg gac aat atc aac cat gtg gca Leu Arg Pro Ser Phe Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala 190 195 200	1227
cag ttc tct tca cgt gga ccg aca aag gat gga cgg atc aaa ccg gat Gln Phe Ser Ser Arg Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp 205 210 215	1275
gtc atg gca ccg gga acg ttc ata cta tca gca aga tct tct ctt gca Val Met Ala Pro Gly Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala 220 225 230 235	1323
ccg gat tcc tcc ttc tgg gcg aac cat gac agt aaa tat gca tac atg Pro Asp Ser Ser Phe Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met 240 245 250	1371
ggt gga acg tcc atg gct aca ccg atc gtt gct gga aac gtg gca cag Gly Gly Thr Ser Met Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln 255 260 265	1419
ctt cgt gag cat ttt gtg aaa aac aga ggc atc aca cca aag cct tct Leu Arg Glu His Phe Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser 270 275 280	1467
cta tta aaa gcg gca ctg att gcc ggt gca gct gac atc ggc ctt ggc Leu Leu Lys Ala Ala Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly 285 290 295	1515
tac ccg aac ggt aac caa gga tgg gga cga gtg aca ttg gat aaa tcc Tyr Pro Asn Gly Asn Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser 300 305 310 315	1563
ctg aac gtt gcc tat gtg aac gag tcc agt tct cta tcc acc agc caa Leu Asn Val Ala Tyr Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln 320 325 330	1611
aaa gcg acg tac tcg ttt act gct act gcc ggc aag cct ttg aaa atc Lys Ala Thr Tyr Ser Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile 335 340 345	1659
tcc ctg gta tgg tct gat gcc cct gcg agc aca act gct tcc gta acg Ser Leu Val Trp Ser Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr 350 355 360	1707

ctt gtc aat gat ctg gac ctt gtc att acc gct cca aat ggc aca cag 1755  
 Leu Val Asn Asp Leu Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln  
 365 370 375

tat gta gga aat gac ttt act tcg cca tac aat gat aac tgg gat ggc 1803  
 Tyr Val Gly Asn Asp Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly  
 380 385 390 395

cgc aat aac gta gaa aat gta ttt att aat gca cca caa agc ggc acg 1851  
 Arg Asn Asn Val Glu Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr  
 400 405 410

tat aca att gag gta cag gct tat aac gta ccg gtt gga cca cag acc 1899  
 Tyr Thr Ile Glu Val Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr  
 415 420 425

ttc tcg ttg gca att gtg aat taa 1923  
 Phe Ser Leu Ala Ile Val Asn  
 430

<210> 3  
 <211> 640  
 <212> PRT  
 <213> Bacillus sp. KSM-KP43

<400> 3

Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala  
 -205 -200 -195

Ala Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly  
 -190 -185 -180

Ala Arg Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr  
 -175 -170 -165

Asp Ala Lys Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala  
 -160 -155 -150

Phe Leu Val Glu Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln  
 -145 -140 -135

Lys Lys Leu Glu Thr Val Pro Ala Asn Asn Lys Leu His Ile Ile  
 -130 -125 -120

Gln Phe Asn Gly Pro Ile Leu Glu Glu Thr Lys Gln Gln Leu Glu  
 -115 -110 -105

Lys Thr Gly Ala Lys Ile Leu Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile  
 -100 -95 -90

Val Glu Tyr Glu Gly Asp Val Lys Ser Ala Thr Ser Thr Ile Glu His

-85		-80		-75		-70									
Val	Glu	Ser	Val	Glu	Pro	Tyr	Leu	Pro	Ile	Tyr	Arg	Ile	Asp	Pro	Gln
				-65					-60					-55	
Leu	Phe	Thr	Lys	Gly	Ala	Ser	Glu	Leu	Val	Lys	Ala	Val	Ala	Leu	Asp
			-50					-45					-40		
Thr	Lys	Gln	Lys	Asn	Lys	Glu	Val	Gln	Leu	Arg	Gly	Ile	Glu	Gln	Ile
		-35					-30					-25			
Ala	Gln	Phe	Ala	Ile	Ser	Asn	Asp	Val	Leu	Tyr	Ile	Thr	Ala	Lys	Pro
	-20					-15					-10				
Glu	Tyr	Lys	Val	Met	Asn	Asp	Val	Ala	Arg	Gly	Ile	Val	Lys	Ala	Asp
-5				-1	1				5					10	
Val	Ala	Gln	Ser	Ser	Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Ile	Val	Ala
			15					20					25		
Val	Ala	Asp	Thr	Gly	Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His
		30					35					40			
Glu	Ala	Phe	Arg	Gly	Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr
	45					50					55				
Asn	Asn	Ala	Asn	Asp	Thr	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser
60					65					70				75	
Val	Leu	Gly	Asn	Gly	Ser	Thr	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn
			80						85					90	
Leu	Val	Phe	Gln	Ser	Ile	Met	Asp	Ser	Gly	Gly	Gly	Leu	Gly	Gly	Leu
			95					100					105		
Pro	Ser	Asn	Leu	Gln	Thr	Leu	Phe	Ser	Gln	Ala	Tyr	Ser	Ala	Gly	Ala
		110					115					120			
Arg	Ile	His	Thr	Asn	Ser	Trp	Gly	Ala	Ala	Val	Asn	Gly	Ala	Tyr	Thr
	125					130					135				
Thr	Asp	Ser	Arg	Asn	Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr
140					145					150					155
Ile	Leu	Phe	Ala	Ala	Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser
			160						165					170	

Ala Pro Gly Thr Ala Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn  
175 180 185

Leu Arg Pro Ser Phe Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala  
190 195 200

Gln Phe Ser Ser Arg Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp  
205 210 215

Val Met Ala Pro Gly Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala  
220 225 230 235

Pro Asp Ser Ser Phe Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met  
240 245 250

Gly Gly Thr Ser Met Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln  
255 260 265

Leu Arg Glu His Phe Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser  
270 275 280

Leu Leu Lys Ala Ala Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly  
285 290 295

Tyr Pro Asn Gly Asn Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser  
300 305 310 315

Leu Asn Val Ala Tyr Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln  
320 325 330

Lys Ala Thr Tyr Ser Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile  
335 340 345

Ser Leu Val Trp Ser Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr  
350 355 360

Leu Val Asn Asp Leu Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln  
365 370 375

Tyr Val Gly Asn Asp Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly  
380 385 390 395

Arg Asn Asn Val Glu Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr  
400 405 410



Tyr Thr Ile Glu Val Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr  
415 420 425

Phe Ser Leu Ala Ile Val Asn  
430

<210> 4  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer 1

<400> 4  
cggacgaata atgccagtga tccgaatggt cat 33

<210> 5  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer 2

<400> 5  
aaaggaatgg cgcctcatgc gaatctagtc ttc 33

<210> 6  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer 3

<400> 6  
ttcagccaag catacagtgc tgggtgccaga att 33

<210> 7  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer 4

<400> 7  
gtcggagcta cggaaagcct ccgcccgaagc ttt 33

<210> 8  
<211> 33  
<212> DNA  
<213> Artificial Sequence

```

<220>
<223> primer 5

<400> 8
atggcaccgg gaacgtacat actatcagca aga 33

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer 6

<400> 9
gccgggtgcag ctgacgtcgg ccttggctac ccg 33

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer 7

<400> 10
ggctacccga acggtagcca aggatgggga cga 33

<210> 11
<211> 1302
<212> DNA
<213> Bacillus sp. KSM-kp9860

<220>
<221> CDS
<222> (1)..(1302)
<223> protease KP9860

<400> 11
aat gat gtg gcc aga ggt att gtg aaa gcg gat gtg gca cag agc agc 48
Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser
1 5 10 15

tac ggt ttg tat gga caa ggc cag att gtc gca gtt gcc gat act gga 96
Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
20 25 30

ttg gat aca gga aga aac gac agt tcg atg cat gaa gcc ttc cgc ggt 144
Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

aaa ata aca gca cta tat gca ctg ggt cgg acg aat aat gcg aat gat 192
Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

acg aac ggt cat ggt acc cat gtg gca ggt tcg gta tta gga aat ggc 240

```

Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly	
65 70 75 80	
gca acg aat aaa gga atg gca cct caa gcg aat ctg gtt ttt caa tcc	288
Ala Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser	
85 90 95	
atc atg gat agc agt ggt ggg ctt gga ggc ttg cct tcc aat ctg caa	336
Ile Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln	
100 105 110	
acc tta ttc agc caa gca ttc agt gca ggt gcc aga att cat aca aac	384
Thr Leu Phe Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn	
115 120 125	
tcc tgg ggg gca gcg gtg aat ggg gcc tac acg aca gat tcc aga aat	432
Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn	
130 135 140	
gtg gat gac tat gta agg aaa aat gat atg acg att ctt ttc gcg gct	480
Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala	
145 150 155 160	
ggg aat gaa ggg ccg aac ggc ggt acc atc agt gca cct ggt acg gct	528
Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala	
165 170 175	
aaa aac gcc atc act gtc ggc gca acc gaa aac ctg cgt cca agc ttc	576
Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe	
180 185 190	
ggg tcc tat gca gat aat att aac cac gtt gca cag ttc tct tcc cgt	624
Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg	
195 200 205	
ggc ccg aca aaa gat ggg cga atc aag cct gat gtc atg gcg cca ggg	672
Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly	
210 215 220	
aca tac att tta tca gca aga tct tct ctt gca ccc gat tcc tcc ttc	720
Thr Tyr Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe	
225 230 235 240	
tgg gcg aat cat gac agc aaa tat gcc tat atg ggt gga acg tcc atg	768
Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met	
245 250 255	
gca aca ccg att gtt gcg ggg aat gtt gca cag ctc cgt gag cat ttt	816
Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe	
260 265 270	
gtg aaa aat aga gga atc act cct aag cct tcc cta ttg aaa gca gct	864
Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala	
275 280 285	
ttg att gca ggt gct gct gat gtt gga ttg ggt tat ccg aac gga aac	912
Leu Ile Ala Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn	
290 295 300	
caa gga tgg ggc cga gtg acc ctg gat aaa tcg ttg aac gtt gcc tat	960
Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr	



Ala Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser  
85 90 95

Ile Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln  
100 105 110

Thr Leu Phe Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn  
115 120 125

Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn  
130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala  
145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala  
165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe  
180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg  
195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly  
210 215 220

Thr Tyr Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe  
225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met  
245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe  
260 265 270

Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala  
275 280 285

Leu Ile Ala Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn  
290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr  
305 310 315 320

Val Asn Glu Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr  
 325 330 335

Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser  
 340 345 350

Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu  
 355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp  
 370 375 380

Phe Ser Ala Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu  
 385 390 395 400

Asn Val Phe Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val  
 405 410 415

Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile  
 420 425 430

Val Asn

<210> 13  
 <211> 1302  
 <212> DNA  
 <213> Bacillus sp. KSM-9865

<220>  
 <221> CDS  
 <222> (1)..(1302)  
 <223> Protease 9865

<400> 13  
 aat gat gtt gca cgt gga att gtc aaa gcg gat gtg gcg cag agc agc 48  
 Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser  
 1 5 10 15  
 tac ggg ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg 96  
 Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly  
 20 25 30  
 ctt gat aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgg ggg 144  
 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly  
 35 40 45  
 aaa att act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat 192  
 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp  
 50 55 60  
 acg aat ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc 240

Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly	
65 70 75 80	
tcc act aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct	288
Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser	
85 90 95	
atc atg gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa	336
Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln	
100 105 110	
acc tta ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac	384
Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn	
115 120 125	
tcc tgg gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat	432
Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn	
130 135 140	
gtg gat gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc	480
Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala	
145 150 155 160	
ggg aat gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct	528
Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala	
165 170 175	
aaa aat gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttc	576
Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe	
180 185 190	
ggg tct tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt	624
Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg	
195 200 205	
gga ccg aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga	672
Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly	
210 215 220	
acg ttc ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc	720
Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe	
225 230 235 240	
tgg gcg aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg	768
Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met	
245 250 255	
gct aca ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt	816
Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe	
260 265 270	
gtg aaa aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca	864
Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala	
275 280 285	
ctg att gcc ggt gca gca gac atc ggc ctt ggc tac ccg aac ggt aac	912
Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn	
290 295 300	
caa gga tgg gga cga gtg aca ttg gat aaa tcc cta aac gtt gcc tat	960
Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr	

305	310	315	320	
gtg aac gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg				1008
Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser				
	325	330	335	
ttt act gct act gcc ggc aag cct ttg aag atc tcc ctg gta tgg tct				1056
Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser				
	340	345	350	
gat gcc cct gcg agc aca act gct tcc gta acg ctt gtc aat gac ctg				1104
Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu				
	355	360	365	
gac ctt gtc att acc gct cca aat ggc aca caa tat gtt gga aat gac				1152
Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp				
	370	375	380	
ttt act tcg cca tac aat aat aac tgg gat ggc cgc aat aac gta gaa				1200
Phe Thr Ser Pro Tyr Asn Asn Asn Trp Asp Gly Arg Asn Asn Val Glu				
	385	390	400	
aat gta ttt att aat gcg cca caa agc ggg acg tat aca att gag gta				1248
Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val				
	405	410	415	
cag gct tat aac gta ccg gtt gga cca cag acc ttc tcg ttg gca att				1296
Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile				
	420	425	430	
gtg aac				1302
Val Asn				

<210> 14  
 <211> 434  
 <212> PRT  
 <213> Bacillus sp. KSM-9865

<400> 14

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser
1 5 10 15

Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
65 70 75 80



Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser  
85 90 95

Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln  
100 105 110

Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn  
115 120 125

Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn  
130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala  
145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala  
165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe  
180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg  
195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly  
210 215 220

Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe  
225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met  
245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe  
260 265 270

Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala  
275 280 285

Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn  
290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr  
305 310 315 320

Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser  
 325 330 335

Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser  
 340 345 350

Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu  
 355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp  
 370 375 380

Phe Thr Ser Pro Tyr Asn Asn Asn Trp Asp Gly Arg Asn Asn Val Glu  
 385 390 395 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val  
 405 410 415

Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile  
 420 425 430

Val Asn

<210> 15  
 <211> 1299  
 <212> DNA  
 <213> Bacillus sp. D-6

<220>  
 <221> CDS  
 <222> (1) .. (1299)  
 <223> Protease E-1

<400> 15	
aat gat gta gca aga gga ata gta aaa gca gac gtt gca caa aac aat	48
Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn	
1 5 10 15	
tac gga cta tat gga caa ggt caa gta gtt gca gta gcg gat acg ggt	96
Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly	
20 25 30	
tta gat aca ggt cgt aac gat agt tct atg cat gaa gca ttc cgt ggg	144
Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly	
35 40 45	
aaa att aca gct ctt tac gcg tta gga aga act aac aat gca aat gat	192
Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp	
50 55 60	
ccg aat ggg cat ggt acg cat gta gct ggt tct gtg ctt ggt aat gct	240

Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Ala		
65					70					75					80		
tta	aat	aaa	gga	atg	gct	ccg	caa	gct	aac	tta	gtc	ttc	caa	tct	att		288
Leu	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	Ile		
				85					90					95			
atg	gat	agc	agc	gga	gga	tta	gga	gga	tta	cca	tcg	aat	tta	aat	acg		336
Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Asn	Thr		
			100					105					110				
tta	ttt	agt	caa	gct	tgg	aat	gct	ggc	gct	aga	att	cat	act	aac	tct		384
Leu	Phe	Ser	Gln	Ala	Trp	Asn	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	Ser		
		115					120					125					
tgg	ggg	gcc	cca	gta	aat	gga	gcg	tac	act	gct	aac	tcg	aga	caa	gtg		432
Trp	Gly	Ala	Pro	Val	Asn	Gly	Ala	Tyr	Thr	Ala	Asn	Ser	Arg	Gln	Val		
	130					135					140						
gat	gag	tat	gtt	cga	aac	aat	gat	atg	acg	gta	ctt	ttt	gca	gct	gga		480
Asp	Glu	Tyr	Val	Arg	Asn	Asn	Asp	Met	Thr	Val	Leu	Phe	Ala	Ala	Gly		
145					150				155						160		
aat	gaa	gga	cct	aac	tct	gga	aca	att	agc	gct	cca	ggg	aca	gcg	aaa		528
Asn	Glu	Gly	Pro	Asn	Ser	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	Lys		
				165					170					175			
aat	gcc	att	acg	gtc	ggc	gca	acg	gaa	aac	tac	cga	cca	agt	ttt	ggt		576
Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Tyr	Arg	Pro	Ser	Phe	Gly		
			180					185					190				
tca	att	gca	gat	aac	cct	aat	cat	atc	gca	caa	ttt	tca	tcg	aga	gga		624
Ser	Ile	Ala	Asp	Asn	Pro	Asn	His	Ile	Ala	Gln	Phe	Ser	Ser	Arg	Gly		
		195					200					205					
gct	acg	aga	gat	gga	cga	att	aaa	cca	gac	gta	aca	gct	cct	gga	aca		672
Ala	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Thr	Ala	Pro	Gly	Thr		
	210					215					220						
ttt	ata	tta	tca	gca	cgc	tct	tct	tta	gca	cca	gac	tct	tcg	ttt	tgg		720
Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp		
225					230					235					240		
gcg	aat	tat	aac	agt	aag	tat	gcg	tat	atg	ggc	ggt	acc	tct	atg	gcg		768
Ala	Asn	Tyr	Asn	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala		
				245					250					255			
aca	cct	ata	gtt	gcg	ggg	aat	gtc	gcg	caa	tta	cgc	gag	cat	ttt	ata		816
Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Ile		
			260					265					270				
aaa	aat	aga	gga	att	aca	cct	aaa	cct	tcc	tta	ata	aaa	gct	gca	ctt		864
Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Ile	Lys	Ala	Ala	Leu		
		275					280					285					
atc	gct	ggg	gct	act	gat	gtt	ggg	tta	gga	tat	cca	agt	ggt	gac	caa		912
Ile	Ala	Gly	Ala	Thr	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Ser	Gly	Asp	Gln		
	290					295					300						
ggc	tgg	ggg	cgt	gtt	act	tta	gat	aaa	tcg	tta	aat	gta	gcg	tat	gtc		960
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val		

305	310	315	320	
aat gaa gca act gca tta aca aca gga caa aaa gca acg tat tcg ttc				1008
Asn Glu Ala Thr Ala Leu Thr Thr Gly Gln Lys Ala Thr Tyr Ser Phe				
325		330	335	
caa acg caa gcg ggt aaa cca tta aaa atc tcg tta gta tgg aca gat				1056
Gln Thr Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp				
340		345	350	
gca cct gga agt aca aca gca tct tat aca cta gtt aat gat tta gat				1104
Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp				
355		360	365	
cta gtt att act gct ccg aat gga caa aaa tat gta ggt aat gat ttt				1152
Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe				
370		375	380	
agt tat cct tat gat aat aat tgg gat ggt cgc aac aat gtt gag aac				1200
Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn				
385		390	400	
gta ttt ata aac gct ccg caa tct gga acg tat aca att gag gtt caa				1248
Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln				
405		410	415	
gcg tat aac gtt cca tct gga cca cag cgt ttc tca cta gct atc gta				1296
Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val				
420		425	430	
cat				1299
His				

<210> 16  
 <211> 433  
 <212> PRT  
 <213> Bacillus sp. D-6

<400> 16

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn			
1	5	10	15
Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly			
20	25	30	
Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly			
35	40	45	
Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp			
50	55	60	
Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala			
65	70	75	80

Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile  
85 90 95

Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr  
100 105 110

Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser  
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val  
130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly  
145 150 155 160

Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys  
165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly  
180 185 190

Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly  
195 200 205

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr  
210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp  
225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala  
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile  
260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu  
275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln  
290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val  
305 310 315 320

Asn Glu Ala Thr Ala Leu Thr Thr Gly Gln Lys Ala Thr Tyr Ser Phe  
 325 330 335

Gln Thr Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp  
 340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp  
 355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe  
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn  
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln  
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val  
 420 425 430

His

<210> 17  
 <211> 1299  
 <212> DNA  
 <213> Bacillus sp. Y

<220>  
 <221> CDS  
 <222> (1)..(1299)  
 <223> Gene name Ya,  
 Protease Ya

<400> 17	
aat gat gta gca aga ggg ata gta aaa gct gat gtt gca caa aac aat	48
Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn	
1 5 10 15	
tac gga tta tat gga caa ggt caa gta gtt gca gta gcg gac aca ggc	96
Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly	
20 25 30	
tta gat aca ggt cgt aac gat agt tct atg cat gaa gca ttc cgc ggg	144
Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly	
35 40 45	
aaa atc aca gct ctt tac gcg tta gga aga act aat aat gcg agt gat	192
Lys Ile Thr Ala Leu Tyr Gln Ala Leu Gly Arg Thr Asn Asn Ala Ser Asp	
50 55 60	

ccg aat ggg cat ggc aca cat gta gca ggt tct gta ctt ggt aat gct	240
Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala	
65 70 75 80	
tta aat aaa gga atg gct ccg caa gct aac tta gtc ttc caa tct att	288
Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile	
85 90 95	
atg gat agc agc gga gga tta ggt ggc tta cca tcg aac tta aat acg	336
Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr	
100 105 110	
tta ttt agt caa gct tgg aat gct gga gca aga att cat act aac tct	384
Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser	
115 120 125	
tgg gga gcc cca gta aat gga gcg tac act gct aac tcg aga caa gtg	432
Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val	
130 135 140	
gat gaa tat gtt cga aat aat gat atg acg gta ctt ttt gca gct ggt	480
Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly	
145 150 155 160	
aat gaa ggt cct aat tca gga aca att agt gct cca ggt aca gcg aaa	528
Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys	
165 170 175	
aat gct att acg gtc ggc gca acg gaa aac tat cgc cca agc ttc ggt	576
Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly	
180 185 190	
tcg ata gca gat aac cca aat cat att gca caa ttt tca tcg aga gga	624
Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly	
195 200 205	
gct acg agg gat gga cga att aag cct gac gta aca gct cct gga aca	672
Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr	
210 215 220	
ttt att tta tca gca cgt tct tcc tta gct cca gac tct tcg ttt tgg	720
Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp	
225 230 235 240	
gcg aat tat aac agt aaa tac gcg tat atg ggc ggt acc tcc atg gcg	768
Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala	
245 250 255	
aca cct att gtt gca ggg aat gtc gcg caa tta cgt gag cat ttt ata	816
Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile	
260 265 270	
aaa aat aga ggt att act cct aag cct tct tta ata aaa gct gca ctt	864
Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu	
275 280 285	
atc gct ggt gct act gat gtt ggt tta gga tat cct aat ggt gac caa	912
Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Asn Gly Asp Gln	
290 295 300	
ggc tgg ggg cgt gtt act cta aat aaa tcg tta aat gta gcg tat gtc	960

[illegible]



Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile  
85 90 95

Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr  
100 105 110

Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser  
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val  
130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly  
145 150 155 160

Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys  
165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly  
180 185 190

Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly  
195 200 205

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr  
210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp  
225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala  
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile  
260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu  
275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Asn Gly Asp Gln  
290 295 300

Gly Trp Gly Arg Val Thr Leu Asn Lys Ser Leu Asn Val Ala Tyr Val  
305 310 315 320

Asn Glu Ala Thr Ala Leu Ala Thr Gly Gln Lys Ala Thr Tyr Ser Phe  
 325 330 335

Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp  
 340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp  
 355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe  
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn  
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Ile Ile Glu Val Gln  
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val  
 420 425 430

His

<210> 19  
 <211> 1299  
 <212> DNA  
 <213> Bacillus SD521

<220>  
 <221> CDS  
 <222> (1)..(1299)  
 <223> Gene name SD-521, protease SD521

<400> 19	
aat gat gta gca aga gga ata gta aaa gca gac gtt gca caa aac aat	48
Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn	
1 5 10 15	
tac gga cta tat gga caa ggt caa gta gtt gca gta gcg gat acg ggt	96
Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly	
20 25 30	
tta gat aca ggt cgt aac gat agt tct atg cat gaa gca ttc cgt ggg	144
Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly	
35 40 45	
aaa att aca gct ctt tac gcg tta gga aga act aac aat gca aat gat	192
Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp	
50 55 60	

ccg aat ggg cat ggt acg cat gta gca ggt tct gta ctt ggt aat gct	240
Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala	
65 70 75 80	
tta aat aaa gga atg gct ccg caa gct aac tta gtc ttc caa tct att	288
Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile	
85 90 95	
atg gat agc agc gga gga tta ggt gga tta cca tcg aat ttg aat acg	336
Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr	
100 105 110	
tta ttt agt caa gct tgg aat gct ggg gct aga att cat act aac tct	384
Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser	
115 120 125	
tgg ggt gct cca gta aat gga gcg tac act gct aac tcg aga caa gtg	432
Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val	
130 135 140	
gat gag tat gtt cga aat aat gat atg acg gta ctt ttt gca gca ggt	480
Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly	
145 150 155 160	
aat gaa ggt cct aat tca gga aca att agt gct cca ggc aca gcg aaa	528
Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys	
165 170 175	
aat gcc att acg gtc ggc gca acg gaa aac tat cgc ccg agc ttc ggt	576
Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly	
180 185 190	
tca tta gca gat aac cca aat cat atc gca caa ttt tca tca aga gga	624
Ser Leu Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly	
195 200 205	
gct acg aga gat gga cga att aaa cca gac gta aca gct cct gga aca	672
Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr	
210 215 220	
ttt att tta tca gca cgt tct tcc tta gcc cca gac tct tcg ttt tgg	720
Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp	
225 230 235 240	
gcg aat tat aac agt aag tat gcg tac atg ggc ggt acc tct atg gcg	768
Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala	
245 250 255	
aca cct ata gtt gcg ggg aat gtc gcg caa tta cgc gag cat ttt ata	816
Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile	
260 265 270	
aaa aat aga gga att aca cct aaa cct tcc tta ata aaa gct gca ctt	864
Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu	
275 280 285	
atc gct ggg gct act gat gtt ggt tta gga tat cca agt ggt gac caa	912
Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln	
290 295 300	
ggc tgg ggg cgt gtt act cta gat aaa tcg tta aat gta gcg tat gtc	960

Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val		
305					310					315					320		
aat	gaa	gca	act	gca	tta	gca	aca	gga	caa	aaa	gca	acg	tat	tcg	ttc	1008	
Asn	Glu	Ala	Thr	Ala	Leu	Ala	Thr	Gly	Gln	Lys	Ala	Thr	Tyr	Ser	Phe		
				325				330					335				
caa	gca	caa	gcg	ggg	aaa	cct	tta	aaa	atc	tcg	tta	gta	tgg	aca	gat	1056	
Gln	Ala	Gln	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Thr	Asp		
			340					345					350				
gca	cct	gga	agt	aca	act	gca	tct	tat	aca	cta	gtt	aat	gat	tta	gat	1104	
Ala	Pro	Gly	Ser	Thr	Thr	Ala	Ser	Tyr	Thr	Leu	Val	Asn	Asp	Leu	Asp		
		355					360					365					
cta	gtt	att	act	gct	ccg	aat	gga	caa	aaa	tat	gta	gga	aat	gat	ttt	1152	
Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Gln	Lys	Tyr	Val	Gly	Asn	Asp	Phe		
	370					375					380						
agt	tat	cct	tat	gat	aat	aac	tgg	gat	ggg	cgc	aac	aat	gtt	gag	aac	1200	
Ser	Tyr	Pro	Tyr	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	Asn		
385					390				395					400			
gta	ttt	ata	aac	gct	ccg	caa	tct	gga	acg	tat	aca	att	gag	gtt	caa	1248	
Val	Phe	Ile	Asn	Ala	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Ile	Glu	Val	Gln		
			405					410					415				
gcg	tat	aat	gta	cca	tct	ggc	cca	cag	cgt	ttc	tca	cta	gct	atc	gta	1296	
Ala	Tyr	Asn	Val	Pro	Ser	Gly	Pro	Gln	Arg	Phe	Ser	Leu	Ala	Ile	Val		
			420					425					430				
cat																1299	
His																	

<210> 20  
 <211> 433  
 <212> PRT  
 <213> Bacillus SD521

<400> 20

Asn	Asp	Val	Ala	Arg	Gly	Ile	Val	Lys	Ala	Asp	Val	Ala	Gln	Asn	Asn		
1				5				10					15				
Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Val	Val	Ala	Val	Ala	Asp	Thr	Gly		
		20					25						30				
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly		
		35					40					45					
Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp		
	50					55				60							
Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Ala		
65					70				75					80			

Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile  
85 90 95

Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr  
100 105 110

Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser  
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val  
130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly  
145 150 155 160

Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys  
165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly  
180 185 190

Ser Leu Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly  
195 200 205

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr  
210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp  
225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala  
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile  
260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu  
275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln  
290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val  
305 310 315 320

Asn Glu Ala Thr Ala Leu Ala Thr Gly Gln Lys Ala Thr Tyr Ser Phe  
 325 330 335

Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp  
 340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp  
 355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe  
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn  
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln  
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val  
 420 425 430

His

<210> 21  
 <211> 1302  
 <212> DNA  
 <213> Bacillus NCIB12289

<220>  
 <221> CDS  
 <222> (1)..(1302)  
 <223> Gene name A1, protease A1

<400> 21	
aac gat gtt gcc aga ggc att gta aaa gcc gat gtt gcc cag agc agc	48
Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser	
1 5 10 15	
tat ggt tta tat ggg caa ggg caa gtg gtt gca gta gcg gat acc gga	96
Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly	
20 25 30	
ctg gat aca ggg cgt aat gac agc tcg atg cat gaa gcg ttc cga gga	144
Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly	
35 40 45	
aag att acc gcg ata tat gcc ctt gga aga aca aac aac gcc aat gat	192
Lys Ile Thr Ala Ile Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp	
50 55 60	

cca aac gga cac ggg acg cat gtt gcc gga tct gtt tta gga aac ggt Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly 65 70 75 80	240
act tcg aat aaa ggg atg gct cca caa gct aac tta gtt ttc caa tct Thr Ser Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser 85 90 95	288
gtt atg gac agc aat ggc gga ctt ggc gga ctg cct tcc aat gta agt Val Met Asp Ser Asn Gly Gly Leu Gly Gly Leu Pro Ser Asn Val Ser 100 105 110	336
aca tta ttc agc cag gca tat agt gcc ggt gcc aga atc cat acg aac Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn 115 120 125	384
tca tgg gga gcg cct gta aac gga gcg tac act act gat tcc aga aac Ser Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn 130 135 140	432
gta gac gat tat gtt cgt aaa aat gat atg gcg gtt ctt ttt gca gcg Val Asp Asp Tyr Val Arg Lys Asn Asp Met Ala Val Leu Phe Ala Ala 145 150 155 160	480
ggt aac gaa ggg ccg aat ggc ggc aca atc agt gct cct ggt acc gcg Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala 165 170 175	528
aag aat gct atc aca gta ggg gca aca gaa aac ctg cgc cca agc ttt Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe 180 185 190	576
gga tct tat gct gac aac atc aat cat gta gca cag ttt tcc tcc cgc Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg 195 200 205	624
gga cct aca aag gat gga cgt atc aaa ccg gac gta atg gca cca gga Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly 210 215 220	672
aca ttt att tta tcg gca aga tct tct ttg gct ccg gac tcc tca ttc Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe 225 230 235 240	720
tgg gca aac cat gac agc aaa tat gct tat atg ggt gga aca tcc atg Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met 245 250 255	768
gcg aca ccg att gta gct ggt aac gtt gca cag tta cgt gaa cat ttc Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe 260 265 270	816
atc aaa aac aga gga atc act cct aaa cca tcc ttg ctg aaa gca gct Ile Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala 275 280 285	864
ctt att gcc gga gca act gat atc ggt ctt ggc tat ccg agt gga aac Leu Ile Ala Gly Ala Thr Asp Ile Gly Leu Gly Tyr Pro Ser Gly Asn 290 295 300	912
caa gga tgg gga aga gta aca ttg gac aag tca ctt aat gta gct ttc	960





Thr Ser Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser  
85 90 95

Val Met Asp Ser Asn Gly Gly Leu Gly Gly Leu Pro Ser Asn Val Ser  
100 105 110

Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn  
115 120 125

Ser Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn  
130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Ala Val Leu Phe Ala Ala  
145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala  
165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe  
180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg  
195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly  
210 215 220

Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe  
225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met  
245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe  
260 265 270

Ile Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala  
275 280 285

Leu Ile Ala Gly Ala Thr Asp Ile Gly Leu Gly Tyr Pro Ser Gly Asn  
290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Phe  
305 310 315 320

Val Asn Glu Thr Ser Ser Leu Ser Thr Asn Gln Lys Ala Thr Tyr Ser  
325 330 335

Phe Thr Ala Gln Ser Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser  
340 345 350

Asp Ala Pro Ala Ser Thr Ser Ala Ser Val Thr Leu Val Asn Asp Leu  
355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp  
370 375 380

Phe Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu  
385 390 395 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val  
405 410 415

Gln Ala Tyr Asn Val Pro Gln Gly Pro Gln Ala Phe Ser Leu Ala Ile  
420 425 430

Val Asn

<210> 23  
<211> 433  
<212> PRT  
<213> Bacillus NCIB12513

<400> 23

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn  
1 5 10 15

Phe Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly  
20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly  
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp  
50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala  
65 70 75 80

Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile

85

90

95

Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ala Asn Leu Gln Thr  
 100 105 110

Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser  
 115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val  
 130 135 140

Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly  
 145 150 155 160

Asn Glu Gly Pro Gly Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys  
 165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly  
 180 185 190

Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly  
 195 200 205

Pro Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr  
 210 215 220

Tyr Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp  
 225 230 235 240

Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala  
 245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val  
 260 265 270

Lys Asn Arg Gly Val Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu  
 275 280 285

Ile Ala Gly Ala Ala Asp Val Gly Leu Gly Phe Pro Asn Gly Asn Gln  
 290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Phe Val  
 305 310 315 320

Asn Glu Thr Ser Pro Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe  
 325 330 335

Thr Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp  
340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Leu Thr Leu Val Asn Asp Leu Asp  
355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp Phe  
370 375 380

Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn  
385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val Gln  
405 410 415

Ala Tyr Asn Val Pro Val Ser Pro Gln Thr Phe Ser Leu Ala Ile Val  
420 425 430

His